

GenCore version 5.1.4\_p5\_4578  
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Database: Nucleic Search, using SW model

Run on: March 29, 2003, 09:34:41, Search time: 81 Seconds

(without alignments) 5084.826 Million cell updates/sec

Title: US-09-750-456-393

Perfect score: 484

Sequence: 1 cctctcttcgcccagagagaga gcatatgacatcagatgacg 484

Scoring table: Identity: 100, Gap: 10

Searched: 574371 seqs, 425486471 residues

Total number of hits satisfying chosen parameters: 1149742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum March 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA:\*

- 1: /cgn2\_6/prodata/1/pubna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/prodata/1/pubna/PC7\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/prodata/1/pubna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/prodata/1/pubna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/prodata/1/pubna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/prodata/1/pubna/PC7\_NEW\_PUBCOMB.seq:\*
- 7: /cgn2\_6/prodata/1/pubna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/prodata/1/pubna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/prodata/1/pubna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/prodata/1/pubna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/prodata/1/pubna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/prodata/1/pubna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/prodata/1/pubna/US09\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/prodata/1/pubna/US06\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match Length | ID   | Description       |
|------------|-------|--------------------|------|-------------------|
| 1          | 475   | 98.1               | 484  | Sequence 103, App |
| 2          | 132.4 | 27.4               | 573  | Sequence 13719, A |
| 3          | 78    | 16.1               | 465  | Sequence 16088, A |
| 4          | 70.4  | 14.5               | 224  | Sequence 27242, A |
| 5          | 45    | 9.3                | 802  | Sequence 312, App |
| 6          | 39.6  | 8.7                | 2892 | Sequence 34, App  |
| 7          | 39.2  | 8.1                | 2692 | Sequence 11, App  |
| 8          | 39    | 8.1                | 8522 | Sequence 3, App   |
| 9          | 38.6  | 8.0                | 2857 | Sequence 36, App  |
| 10         | 36.6  | 7.6                | 1981 | Sequence 5, App   |
| 11         | 36.6  | 7.6                | 2663 | Sequence 8, App   |
| 12         | 36.6  | 7.6                | 2933 | Sequence 445, App |
| 13         | 36.6  | 7.6                | 2933 | Sequence 345, App |
| 14         | 36.6  | 7.6                | 2933 | Sequence 345, App |
| 15         | 36.6  | 7.6                | 2933 | Sequence 345, App |
| 16         | 36.6  | 7.6                | 2933 | Sequence 345, App |
| 17         | 36.6  | 7.6                | 2933 | Sequence 345, App |
| 18         | 36.6  | 7.6                | 2933 | Sequence 345, App |
| 19         | 36.6  | 7.6                | 2933 | Sequence 345, App |
| 20         | 36.6  | 7.6                | 2933 | Sequence 345, App |

|    |      |     |       |                    |                    |
|----|------|-----|-------|--------------------|--------------------|
| 20 | 36.6 | 7.6 | 2933  | US-10-137-865-345  | Sequence 345, App  |
| 21 | 36.6 | 7.6 | 2933  | US-10-140-474-345  | Sequence 345, App  |
| 22 | 36.6 | 7.6 | 2933  | US-10-143-431-345  | Sequence 345, App  |
| 23 | 36.6 | 7.6 | 2933  | US-10-143-114-345  | Sequence 345, App  |
| 24 | 36.6 | 7.6 | 2933  | US-10-140-002-345  | Sequence 345, App  |
| 25 | 36.6 | 7.6 | 2933  | US-10-140-410-345  | Sequence 345, App  |
| 26 | 36.6 | 7.6 | 2933  | US-10-137-022-345  | Sequence 345, App  |
| 27 | 36.6 | 7.6 | 2933  | US-10-147-423-345  | Sequence 345, App  |
| 28 | 36.6 | 7.6 | 2933  | US-10-121-050-345  | Sequence 345, App  |
| 29 | 36.6 | 7.6 | 2933  | US-10-141-785-345  | Sequence 345, App  |
| 30 | 36.6 | 7.6 | 2933  | US-09-828-366-320  | Sequence 345, App  |
| 31 | 35.8 | 7.4 | 464   | US-09-831-381-1517 | Sequence 147, App  |
| 32 | 34.8 | 7.2 | 14917 | US-09-908-567B-11  | Sequence 11, App   |
| 33 | 34.8 | 7.0 | 882   | US-10-184-644-574  | Sequence 574, App  |
| 34 | 33.8 | 7.0 | 2933  | US-09-854-456-552  | Sequence 552, App  |
| 35 | 33.8 | 7.0 | 2933  | US-09-857-701-9716 | Sequence 9716, App |
| 36 | 33.8 | 7.0 | 2933  | US-09-857-701-9716 | Sequence 9716, App |
| 37 | 33.4 | 6.9 | 11648 | US-10-149-819-42   | Sequence 42, App   |
| 38 | 33.2 | 6.9 | 571   | US-10-184-644-345  | Sequence 345, App  |
| 39 | 33.2 | 6.9 | 5670  | US-09-954-456-1146 | Sequence 1146, App |
| 40 | 32.8 | 6.8 | 330   | US-09-857-701-9716 | Sequence 9716, App |
| 41 | 32.6 | 6.7 | 62804 | US-10-896-360-3    | Sequence 3, App    |
| 42 | 32.2 | 6.7 | 406   | US-09-857-701-9716 | Sequence 9716, App |
| 43 | 32.2 | 6.7 | 772   | US-09-857-701-9716 | Sequence 9716, App |
| 44 | 32.2 | 6.7 | 1057  | US-09-831-381-1517 | Sequence 1517, App |
| 45 | 32   | 6.6 | 7332  | US-03-944-849-1    | Sequence 1, App    |

## ALIGNMENTS

RESULT 1  
US-09-728-445-393  
Sequence: 103 Application US/09728445  
Patient: NA US090910254AI  
GENERAL INFORMATION:  
APPLICANT: Friedrich, Glenn  
APPLICANT: Cambricowicz, Brian  
APPLICANT: Sands, Arthur T.  
TITLE OF INVENTION: No US090910254AI Mutated Maternal Cell and  
FILE REFERENCE: LEX 0102-USA  
CURRENT APPLICATION NUMBER: US/01/728-445  
CURRENT FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/168,358  
ERROR FILING DATE: 1999-10-01  
NUMBER OF SEQ ID NOS: 891  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 393  
LENGTH: 484  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: (1) (484)  
OTHER INFORMATION: n = A,T,C or G  
US-09-728-445-393

Query Match: 98.1% Score 475, DP 103, Length 484  
Best local similarity: 100.0%, Pred No: 7,000,132, Indels 0, Gaps 0  
Matches 484, Conservative 0, Mismatches 0, Indels 0, Gaps 0

1 cctctcttcgcccagagagaga gcatatgacatcagatgacg 60  
2 cctctcttcgcccagagagaga gcatatgacatcagatgacg 60  
3 cctctcttcgcccagagagaga gcatatgacatcagatgacg 60  
4 cctctcttcgcccagagagaga gcatatgacatcagatgacg 60  
5 cctctcttcgcccagagagaga gcatatgacatcagatgacg 60  
6 cctctcttcgcccagagagaga gcatatgacatcagatgacg 60  
7 cctctcttcgcccagagagaga gcatatgacatcagatgacg 60  
8 cctctcttcgcccagagagaga gcatatgacatcagatgacg 60  
9 cctctcttcgcccagagagaga gcatatgacatcagatgacg 60  
10 cctctcttcgcccagagagaga gcatatgacatcagatgacg 60  
11 cctctcttcgcccagagagaga gcatatgacatcagatgacg 60  
12 cctctcttcgcccagagagaga gcatatgacatcagatgacg 60  
13 cctctcttcgcccagagagaga gcatatgacatcagatgacg 60  
14 cctctcttcgcccagagagaga gcatatgacatcagatgacg 60  
15 cctctcttcgcccagagagaga gcatatgacatcagatgacg 60  
16 cctctcttcgcccagagagaga gcatatgacatcagatgacg 60  
17 cctctcttcgcccagagagaga gcatatgacatcagatgacg 60  
18 cctctcttcgcccagagagaga gcatatgacatcagatgacg 60  
19 cctctcttcgcccagagagaga gcatatgacatcagatgacg 60  
20 cctctcttcgcccagagagaga gcatatgacatcagatgacg 60







|                       |        |                 |        |              |
|-----------------------|--------|-----------------|--------|--------------|
| Query Match           | 8.0%   | Score 38.6;     | DB 10; | Length 2857; |
| Best Local Similarity | 62.8%; | Prd'd No 0.037; |        |              |
| Matches               | 59;    | Conservative    | 35;    | Indels 0;    |
|                       |        | Mismatches      |        | Gaps 0;      |











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